## ABSTRACT

The present invention presents methods for gene expression monitoring that utilize microelectronic arrays to drive the transport and hybridization of nucleic acids. Procedures are described for generating mRNA expression samples for use in these methods from populations of cells, tissues, or other biological source materials, that may differ in their physiological and/or pathological state. Provided in the invention are methods for generating a reusable nucleic acid transcript library from mRNA in a sample of biological material. In order to improve gene expression monitoring on the microelectronic arrays, the transcripts are amplified to produce sample nucleic acid amplicons of a defined length. Because multiple sample amplicons may be selectively hybridized to controlled sites in the electronic array, the gene expression profiles of the polynucleotide populations from different sources can be directly compared in an array format using electronic hybridization methodologies. Also provided in the invention are methods for detecting the level of sample amplicons using electronically assisted primer extension detection, and utilizing individual test site hybridization controls. The hybridization data collected utilizing the improved methods of the present invention will allow the correlation of changes in mRNA level with the corresponding expression of the encoded protein in the biological source material, and thus aid in studying the role of gene expression in disease.